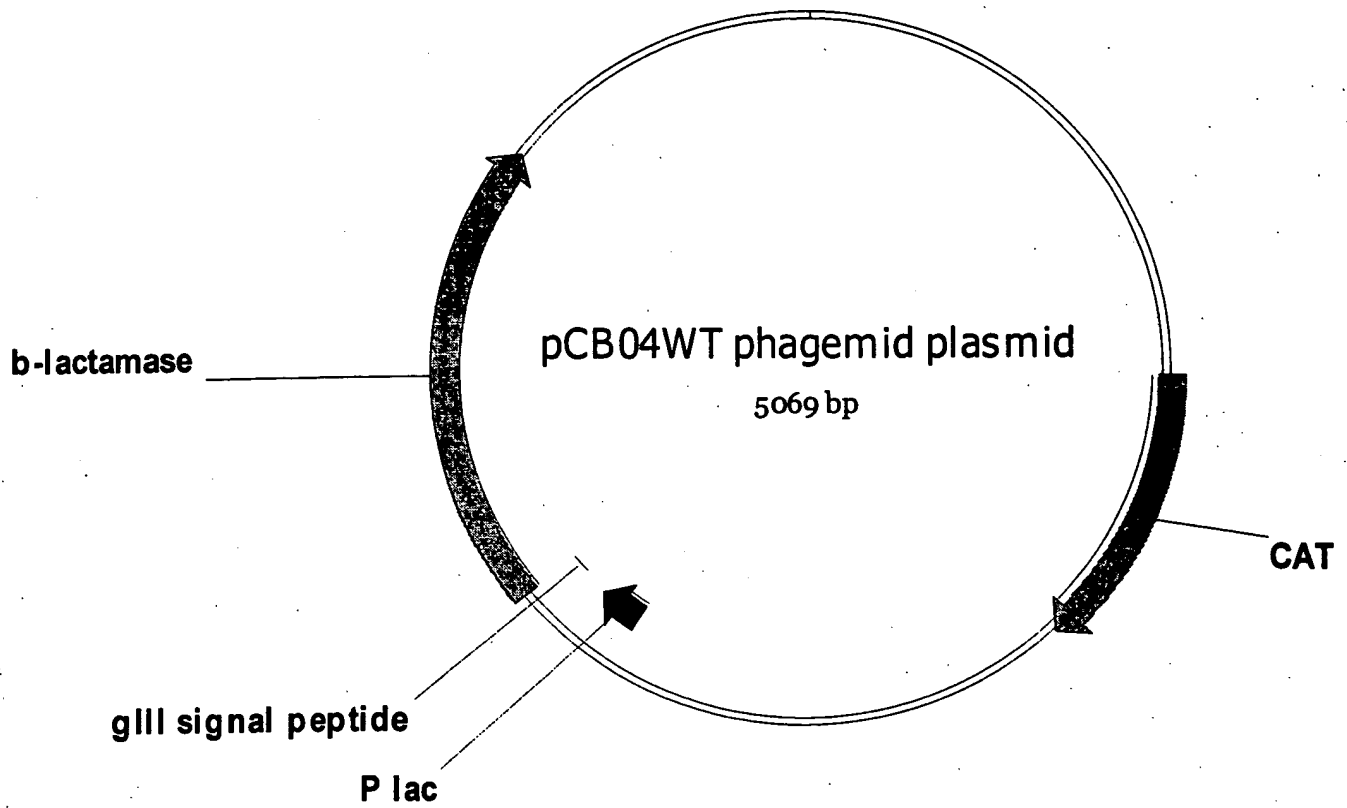


FIGURE 1.



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FIGURE 3.

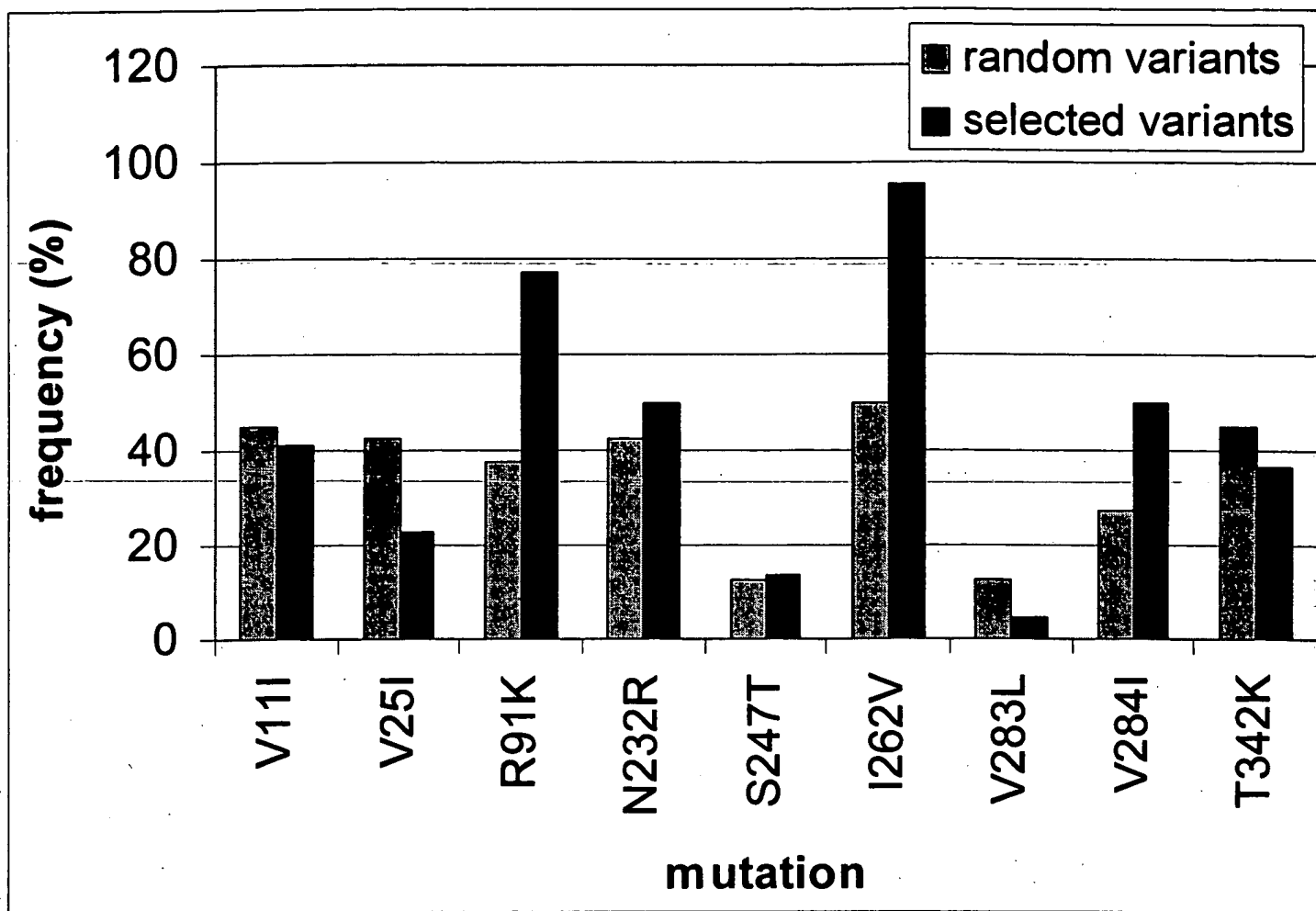
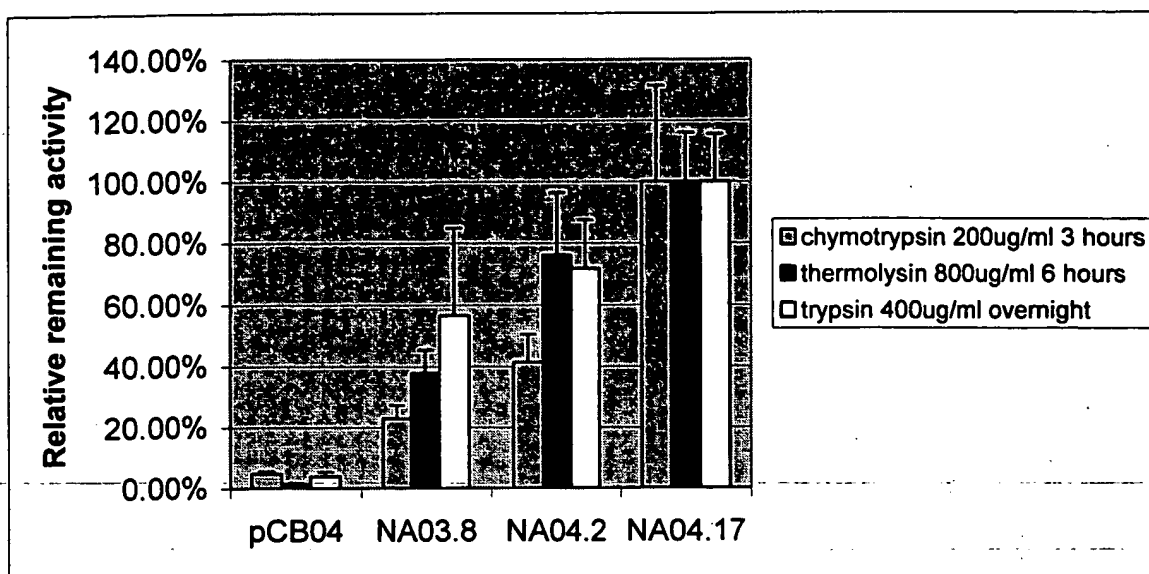


FIGURE 4.

aa change	parameter	# occur.	rank
T1A	0.100	0	
S4T	0.050	4	14
V11I	0.375	4	5
A13D	0.036	4	15
V25I	0.194	2	9
Y41F	-0.232	7	24
F43Y	-0.092	5	18
I65V	-0.219	20	22
R91K	0.367	2	6
Q95E	0.756	9	1
R105T	-0.223	2	23
M106L	-0.175	3	20
S130A	-0.102	14	19
A153S	0.669	10	2
Y170F	-0.256	4	25
A194S	0.141	4	12
A208P	-0.021	8	16
Q219E	-0.446	8	28
T225S	0.172	3	11
N226T	-0.198	8	21
V227A	-0.311	6	27
N232R	0.442	6	3
S247T	0.177	4	10
I262V	0.294	15	8
V283L	0.334	3	7
V284I	0.378	19	4
P295A	-0.299	5	26
I334L	-0.062	6	17
T342K	0.107	9	13
const. C	0.471		

FIGURE 5.



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FIGURE 6.

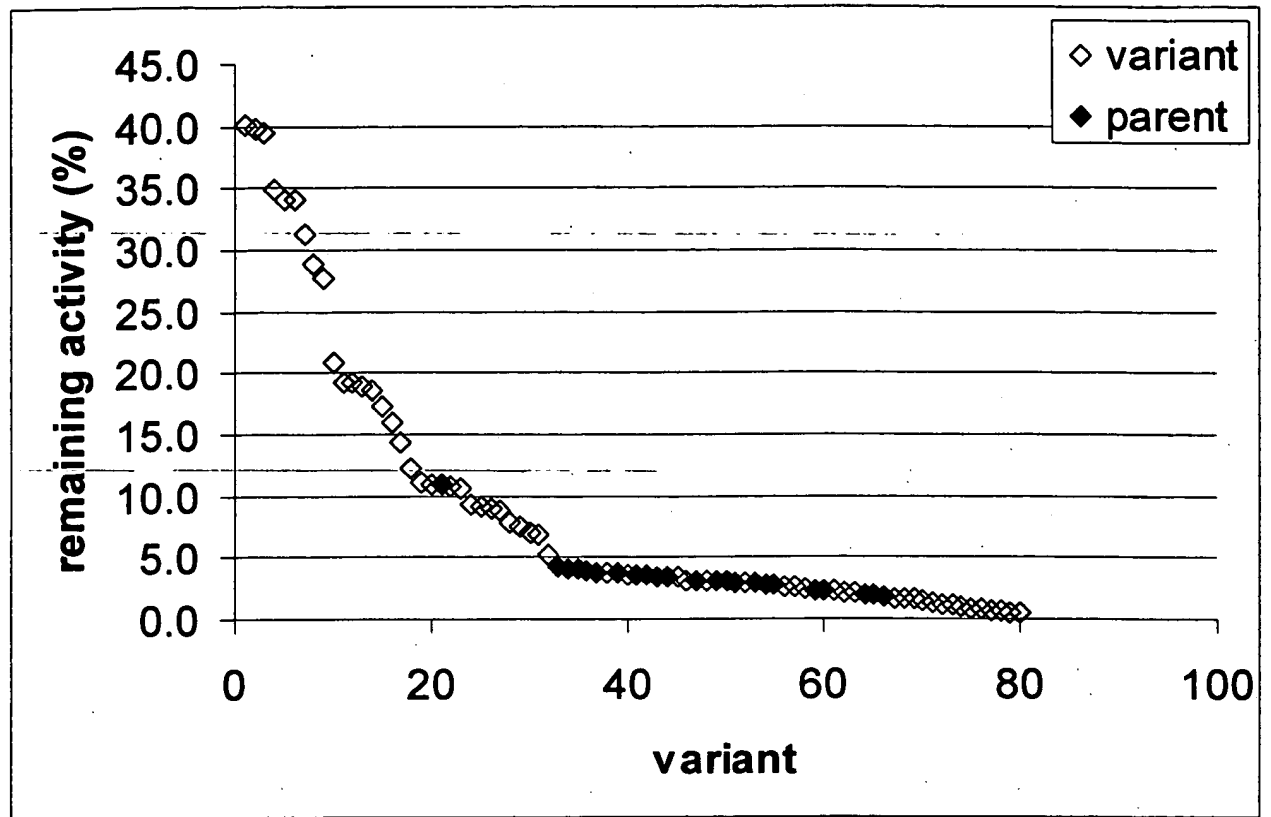


FIGURE 7.

heavy chain:

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vss (SEQ ID NO:2)

linker:

Gggsgggsgggsggs (SEQ ID NO:3)

light chain:

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ID NO:4)

BLA:

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FIGURE 8.

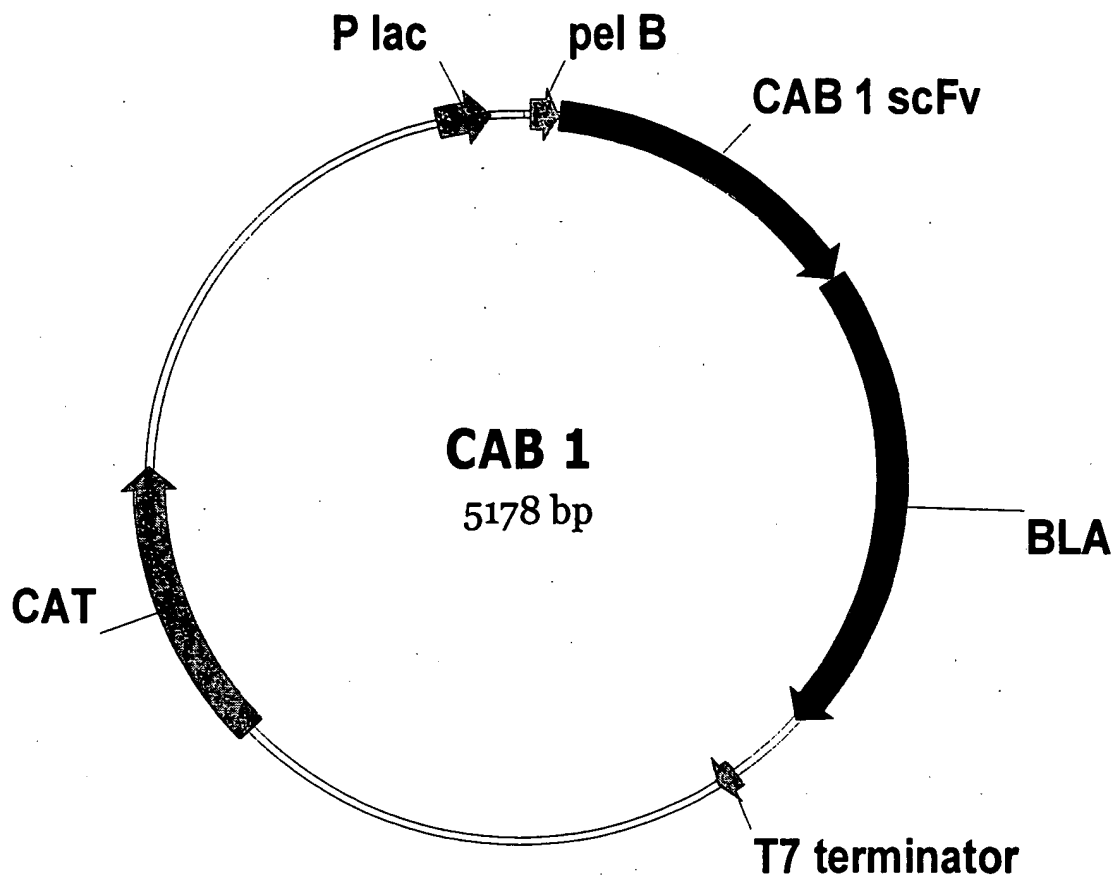
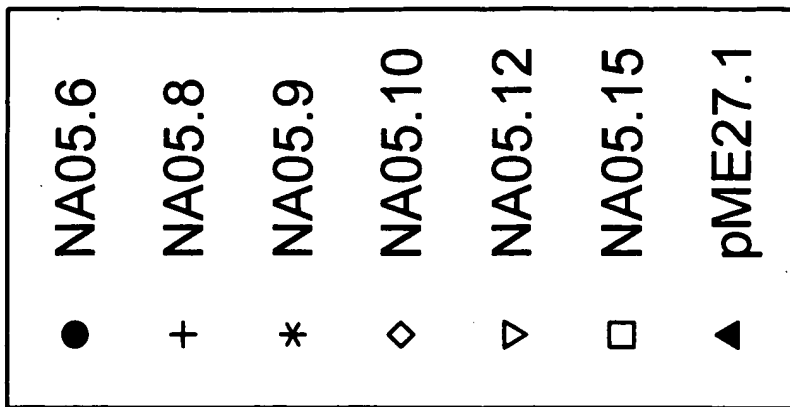


FIGURE 9.

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FIGURE 10.

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		TFS V A G
		KP G
		Q
81	Translation of CAB1	160
(81)	human consensus	(81) LQLSSLTSEDVAVYYCNEGTPGYPYFDYWGQGTVTTVSSGGGGGGGGGSENVLTSQPAIMASPGKVTITCSA (SEQ ID NO:7)
		QS P S V QT
		AR
161	Translation of CAB1	240
(161)	human consensus	(161) SSSVSYMHWFQOKPGTSPKLMWIYSTSNLASGVPARFSGSGSGTSYSLTISRMEAEADAATYYCQQRSSYPPLTFGAGTKLELKRAA (SEQ ID NO:8)
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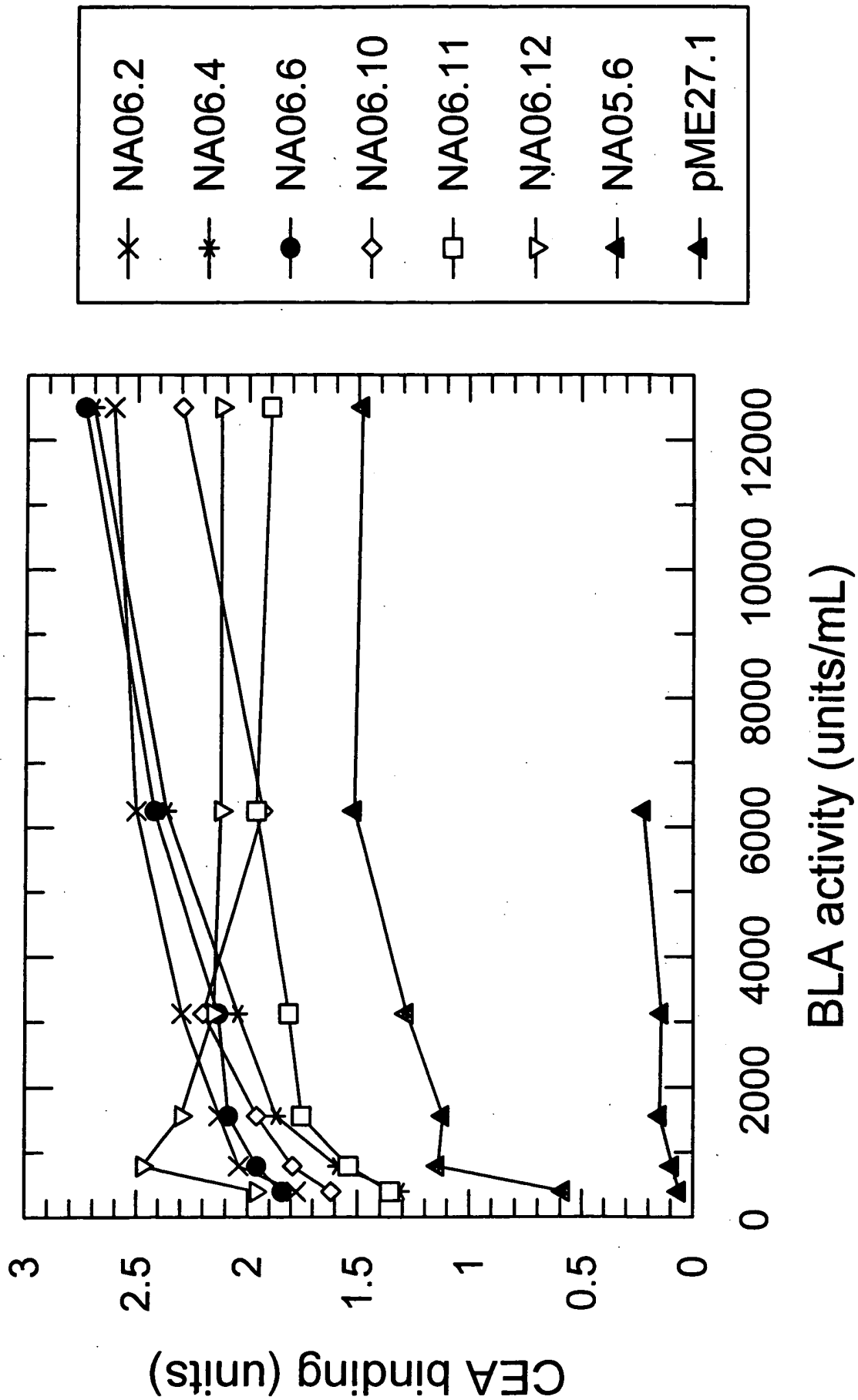


FIGURE 13.

